

# SEQUENCE LISTING

<110> Caput, Daniel  
 Ferrara, Pascual  
 Kaghad, Ahmed Mourad

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<140> 09/125,005

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<150> PCT/FR97/00214

<151> 1997-02-03

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<170> PatentIn Ver. 2.0

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FEB 01 2000

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 Met Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro  
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 485 490 495  
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Val His Gly Gly Val Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly  
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	10 15 20	
CCA GAC AGC ACC TAC TTC GAC CTT CCC CAG TCA AGC CGG GGG AAT AAT	149	
Pro Asp Ser Thr Tyr Phe Asp Leu Pro Gln Ser Ser Arg Gly Asn Asn		
	25 30 35	
GAG GTG GTG GGC GGA ACG GAT TCC AGC ATG GAC GTC TTC CAC CTG GAG	197	
Glu Val Val Gly Gly Thr Asp Ser Ser Met Asp Val Phe His Leu Glu		
	40 45 50 55	
GGC ATG ACT ACA TCT GTC ATG GCC CAG TTC AAT CTG CTG AGC AGC ACC	245	
Gly Met Thr Thr Ser Val Met Ala Gln Phe Asn Leu Leu Ser Ser Thr		
	60 65 70	
ATG GAC CAG ATG AGC AGC CGC GCG GCC TCG GCC AGC CCC TAC ACC CCA	293	
Met Asp Gln Met Ser Ser Arg Ala Ala Ser Ala Ser Pro Tyr Thr Pro		
	75 80 85	
GAG CAC GCC GCC AGC GTG CCC ACC CAC TCG CCC TAC GCA CAA CCC AGC	341	
Glu His Ala Ala Ser Val Pro Thr His Ser Pro Tyr Ala Gln Pro Ser		
	90 95 100	
TCC ACC TTC GAC ACC ATG TCG CCG GCG CCT GTC ATC CCC TCC AAC ACC	389	
Ser Thr Phe Asp Thr Met Ser Pro Ala Pro Val Ile Pro Ser Asn Thr		
	105 110 115	
GAC TAC CCC GGA CCC CAC CAC TTT GAG GTC ACT TTC CAG CAG TCC AGC	437	
Asp Tyr Pro Gly Pro His His Phe Glu Val Thr Phe Gln Gln Ser Ser		
	120 125 130 135	
ACG GCC AAG TCA GCC ACC TGG ACG TAC TCC CCG CTC TTG AAG AAA CTC	485	
Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Pro Leu Leu Lys Lys Leu		
	140 145 150	
TAC TGC CAG ATC GCC AAG ACA TGC CCC ATC CAG ATC AAG GTG TCC ACC	533	
Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys Val Ser Thr		
	155 160 165	
CCG CCA CCC CCA GGC ACT GCC ATC CGG GCC ATG CCT GTT TAC AAG AAA	581	
Pro Pro Pro Pro Gly Thr Ala Ile Arg Ala Met Pro Val Tyr Lys Lys		
	170 175 180	
GCG GAG CAC GTG ACC GAC GTC GTG AAA CGC TGC CCC AAC CAC GAG CTC	629	
Ala Glu His Val Thr Asp Val Val Lys Arg Cys Pro Asn His Glu Leu		
	185 190 195	
GGG AGG GAC TTC AAC GAA GGA CAG TCT GCT CCA GCC AGC CAC CTC ATC	677	
Gly Arg Asp Phe Asn Glu Gly Gln Ser Ala Pro Ala Ser His Leu Ile		

45A

200	205	210	215	
CGC GTG GAA GGC AAT AAT CTC TCG CAG TAT GTG GAT GAC CCT GTC ACC Arg Val Glu Gly Asn Asn Leu Ser Gln Tyr Val Asp Asp Pro Val Thr	220	225	230	725
GGC AGG CAG AGC GTC GTG GTG CCC TAT GAG CCA CCA CAG GTG GGG ACG Gly Arg Gln Ser Val Val Val Pro Tyr Glu Pro Pro Gln Val Gly Thr	235	240	245	773
GAA TTC ACC ACC ATC CTG TAC AAC TTC ATG TGT AAC AGC AGC TGT GTA Glu Phe Thr Thr Ile Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val	250	255	260	821
GGG GGC ATG AAC CGG CGG CCC ATC CTC ATC ATC ATC ACC CTG GAG ATG Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Ile Thr Leu Glu Met	265	270	275	869
CGG GAT GGG CAG GTG CTG GGC CGC CGG TCC TTT GAG GGC CGC ATC TGC Arg Asp Gly Gln Val Leu Gly Arg Arg Ser Phe Glu Gly Arg Ile Cys	280	285	290	917
GCC TGT CCT GGC CGC GAC CGA AAA GCT GAT GAG GAC CAC TAC CGG GAG Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp His Tyr Arg Glu	300	305	310	965
CAG CAG GCC CTG AAC GAG AGC TCC GCC AAG AAC GGG GCC GCC AGC AAG Gln Gln Ala Leu Asn Glu Ser Ser Ala Lys Asn Gly Ala Ala Ser Lys	315	320	325	1013
CGT GCC TTC AAG CAG AGC CCC CCT GCC GTC CCC GCC CTT GGT GCC GGT Arg Ala Phe Lys Gln Ser Pro Pro Ala Val Pro Ala Leu Gly Ala Gly	330	335	340	1061
GTG AAG AAG CGG CGG CAT GGA GAC GAG GAC ACG TAC TAC CTT CAG GTG Val Lys Lys Arg Arg His Gly Asp Glu Asp Thr Tyr Tyr Leu Gln Val	345	350	355	1109
CGA GGC CGG GAG AAC TTT GAG ATC CTG ATG AAG CTG AAA GAG AGC CTG Arg Gly Arg Glu Asn Phe Glu Ile Leu Met Lys Leu Lys Glu Ser Leu	360	365	370	1157
GAG CTG ATG GAG TTG GTG CCG CAG CCA CTG GTG GAC TCC TAT CGG CAG Glu Leu Met Glu Leu Val Pro Gln Pro Leu Val Asp Ser Tyr Arg Gln	380	385	390	1205
CAG CAG CAG CTC CTA CAG AGG CCG AGT CAC CTA CAG CCC CCG TCC TAC Gln Gln Gln Leu Leu Gln Arg Pro Ser His Leu Gln Pro Pro Ser Tyr	395	400	405	1253
GGG CCG GTC CTC TCG CCC ATG AAC AAG GTG CAC GGG GGC ATG AAC AAG Gly Pro Val Leu Ser Pro Met Asn Lys Val His Gly Gly Met Asn Lys	410	415	420	1301
CTG CCC TCC GTC AAC CAG CTG GTG GGC CAG CCT CCC CCG CAC AGT TCG Leu Pro Ser Val Asn Gln Leu Val Gly Gln Pro Pro Pro His Ser Ser	425	430	435	1349

AS  
mt

GCA GCT ACA CCC AAC CTG GGG CCC GTG GGC CCC GGG ATG CTC AAC AAC Ala Ala Thr Pro Asn Leu Gly Pro Val Gly Pro Gly Met Leu Asn Asn 440 445 450 455	1397
CAT GGC CAC GCA GTG CCA GCC AAC GGC GAG ATG AGC AGC AGC CAC AGC His Gly His Ala Val Pro Ala Asn Gly Glu Met Ser Ser Ser His Ser 460 465 470	1445
GCC CAG TCC ATG GTC TCG GGG TCC CAC TGC ACT CCG CCA CCC CCC TAC Ala Gln Ser Met Val Ser Gly Ser His Cys Thr Pro Pro Pro Pro Tyr 475 480 485	1493
CAC GCC GAC CCC AGC CTC GTC AGT TTT TTA ACA GGA TTG GGG TGT CCA His Ala Asp Pro Ser Leu Val Ser Phe Leu Thr Gly Leu Gly Cys Pro 490 495 500	1541
AAC TGC ATC GAG TAT TTC ACC TCC CAA GGG TTA CAG AGC ATT TAC CAC Asn Cys Ile Glu Tyr Phe Thr Ser Gln Gly Leu Gln Ser Ile Tyr His 505 510 515	1589
CTG CAG AAC CTG ACC ATT GAG GAC CTG GGG GCC CTG AAG ATC CCC GAG Leu Gln Asn Leu Thr Ile Glu Asp Leu Gly Ala Leu Lys Ile Pro Glu 520 525 530 535	1637
CAG TAC CGC ATG ACC ATC TGG CGG GGC CTG CAG GAC CTG AAG CAG GGC Gln Tyr Arg Met Thr Ile Trp Arg Gly Leu Gln Asp Leu Lys Gln Gly 540 545 550	1685
CAC GAC TAC AGC ACC GCG CAG CAG CTG CTC CGC TCT AGC AAC GCG GCC His Asp Tyr Ser Thr Ala Gln Gln Leu Leu Arg Ser Ser Asn Ala Ala 555 560 565	1733
ACC ATC TCC ATC GGC GGC TCA GGG GAA CTG CAG CGC CAG CGG GTC ATG Thr Ile Ser Ile Gly Gly Ser Gly Glu Leu Gln Arg Gln Arg Val Met 570 575 580	1781
GAG GCC GTG CAC TTC CGC GTG CGC CAC ACC ATC ACC ATC CCC AAC CGC Glu Ala Val His Phe Arg Val Arg His Thr Ile Thr Ile Pro Asn Arg 585 590 595	1829
GGC GGC CCA GGC GGC GGC CCT GAC GAG TGG GCG GAC TTC GGC TTC GAC Gly Gly Pro Gly Gly Gly Pro Asp Glu Trp Ala Asp Phe Gly Phe Asp 600 605 610 615	1877
CTG CCC GAC TGC AAG GCC CGC AAG CAG CCC ATC AAG GAG GAG TTC ACG Leu Pro Asp Cys Lys Ala Arg Lys Gln Pro Ile Lys Glu Glu Phe Thr 620 625 630	1925
GAG GCC GAG ATC CAC TGAGGGCCTC GCCTGGCTGC AGCCTGCGCC ACCGCCCAGA Glu Ala Glu Ile His 635	1980
GACCCAAGCT GCCTCCCCTC TCCTTCCTGT GTGTCCAAAA CTGCCTCAGG AGGCAGGACC	2040
TTCTGGGCTGT GCCCGGGGAA AGGCAAGGTC CGGCCCATCC CCAGGCACCT CACAGGCCCC	2100

AS  
64

AGGAAAGGCC CAGCCACCGA AGCCGCCTGT GGACAGCCTG AGTCACCTGC AGAACC

2156

&lt;210&gt; 6

&lt;211&gt; 636

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 6

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His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro  
20 25 30

Gln Ser Ser Arg Gly Asn Asn Glu Val Val Gly Gly Thr Asp Ser Ser  
35 40 45

Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln  
50 55 60

Phe Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala  
65 70 75 80

Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His  
85 90 95

Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala  
100 105 110

Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu  
115 120 125

Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr  
130 135 140

Ser Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro  
145 150 155 160

Ile Gln Ile Lys Val Ser Thr Pro Pro Pro Gly Thr Ala Ile Arg  
165 170 175

Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys  
180 185 190

Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser  
195 200 205

Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln  
210 215 220

Tyr Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr  
225 230 235 240

Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe  
245 250 255

AS  
W

Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu  
 260 265 270  
 Ile Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg  
 275 280 285  
 Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala  
 290 295 300  
 Asp Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala  
 305 310 315 320  
 Lys Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala  
 325 330 335  
 Val Pro Ala Leu Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu  
 340 345 350  
 Asp Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu  
 355 360 365  
 Met Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro  
 370 375 380  
 Leu Val Asp Ser Tyr Arg Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser  
 385 390 395 400  
 His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys  
 405 410 415  
 Val His Gly Gly Met Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly  
 420 425 430  
 Gln Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val  
 435 440 445  
 Gly Pro Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Gly  
 450 455 460  
 Glu Met Ser Ser Ser His Ser Ala Gln Ser Met Val Ser Gly Ser His  
 465 470 475 480  
 Cys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe  
 485 490 495  
 Leu Thr Gly Leu Gly Cys Pro Asn Cys Ile Glu Tyr Phe Thr Ser Gln  
 500 505 510  
 Gly Leu Gln Ser Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp Leu  
 515 520 525  
 Gly Ala Leu Lys Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly  
 530 535 540  
 Leu Gln Asp Leu Lys Gln Gly His Asp Tyr Ser Thr Ala Gln Gln Leu  
 545 550 555 560

AS  
 wt



Leu Arg Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu  
565 570 575

Leu Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His  
580 585 590

Thr Ile Thr Ile Pro Asn Arg Gly Gly Pro Gly Gly Gly Pro Asp Glu  
595 600 605

Trp Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys Gln  
610 615 620

Pro Ile Lys Glu Glu Phe Thr Glu Ala Glu Ile His  
625 630 635

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<400> 7

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GACACCCAAG GAAACCTTGC TGGCTTTGAG AAAGGGATCG TCTCTCTCCT GCCCAAGAGA 120

AGC ATG TGT ATG GGC CCT GTG TAT GAA TCC TTG GGG CAG GCC CAG TTC 168  
Met Cys Met Gly Pro Val Tyr Glu Ser Leu Gly Gln Ala Gln Phe  
1 5 10 15

AAT TTG CTC AGC AGT GCC ATG GAC CAG ATG GGC AGC CGT GCG GCC CCG 216  
Asn Leu Leu Ser Ser Ala Met Asp Gln Met Gly Ser Arg Ala Ala Pro  
20 25 30

GCG AGC CCC TAC ACC CCG GAG CAC GCC GCC AGC GCG CCC ACC CAC TCG 264  
Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Ala Pro Thr His Ser  
35 40 45

CCC TAC GCG CAG CCC AGC TCC ACC TTC GAC ACC ATG TCT CCG GCG CCT 312  
Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro  
50 55 60

GTC ATC CCT TCC AAT ACC GAC TAC CCC GGC CCC CAC CAC TTC GAG GTC 360  
Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu Val  
65 70 75

ACC TTC CAG CAG TCG AGC ACT GCC AAG TCG GCC ACC TGG ACA TAC TCC 408  
Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser  
80 85 90 95

CCA CTC TTG AAG AAG TTG TAC TGT CAG ATT GCT AAG ACA TGC CCC ATC 456

AS  
cut

Pro	Leu	Leu	Lys	Lys	Leu	Tyr	Cys	Gln	Ile	Ala	Lys	Thr	Cys	Pro	Ile	
				100					105					110		
CAG	ATC	AAA	GTG	TCC	ACA	CCA	CCA	CCC	CCG	GGC	ACG	GCC	ATC	CGG	GCC	504
Gln	Ile	Lys	Val	Ser	Thr	Pro	Pro	Pro	Pro	Gly	Thr	Ala	Ile	Arg	Ala	
			115					120				125				
ATG	CCT	GTC	TAC	AAG	AAG	GCA	GAG	CAT	GTG	ACC	GAC	ATT	GTT	AAG	CGC	552
Met	Pro	Val	Tyr	Lys	Lys	Ala	Glu	His	Val	Thr	Asp	Ile	Val	Lys	Arg	
		130					135				140					
TGC	CCC	AAC	CAC	GAG	CTT	GGA	AGG	GAC	TTC	AAT	GAA	GGA	CAG	TCT	GCC	600
Cys	Pro	Asn	His	Glu	Leu	Gly	Arg	Asp	Phe	Asn	Glu	Gly	Gln	Ser	Ala	
	145					150					155					
CCG	GCT	AGC	CAC	CTC	ATC	CGT	GTA	GAA	GGC	AAC	AAC	CTC	GCC	CAG	TAC	648
Pro	Ala	Ser	His	Leu	Ile	Arg	Val	Glu	Gly	Asn	Asn	Leu	Ala	Gln	Tyr	
160					165				170					175		
GTG	GAT	GAC	CCT	GTC	ACC	GGA	AGG	CAG	AGT	GTG	GTT	GTG	CCG	TAT	GAA	696
Val	Asp	Asp	Pro	Val	Thr	Gly	Arg	Gln	Ser	Val	Val	Val	Pro	Tyr	Glu	
				180				185						190		
CCC	CCA	CAG	GTG	GGA	ACA	GAA	TTT	ACC	ACC	ATC	CTG	TAC	AAC	TTC	ATG	744
Pro	Pro	Gln	Val	Gly	Thr	Glu	Phe	Thr	Thr	Ile	Leu	Tyr	Asn	Phe	Met	
			195					200					205			
TGT	AAC	AGC	AGC	TGT	GTG	GGG	GGC	ATG	AAT	CGG	AGG	CCC	ATC	CTT	GTC	792
Cys	Asn	Ser	Ser	Cys	Val	Gly	Gly	Met	Asn	Arg	Arg	Pro	Ile	Leu	Val	
		210					215					220				
ATC	ATC	ACC	CTG	GAG	ACC	CGG	GAT	GGA	CAG	GTC	CTG	GGC	CGC	CGG	TCT	840
Ile	Ile	Thr	Leu	Glu	Thr	Arg	Asp	Gly	Gln	Val	Leu	Gly	Arg	Arg	Ser	
	225					230					235					
TTC	GAG	GGT	CGC	ATC	TGT	GCC	TGT	CCT	GGC	CGT	GAC	CGC	AAA	GCT	GAT	888
Phe	Glu	Gly	Arg	Ile	Cys	Ala	Cys	Pro	Gly	Arg	Asp	Arg	Lys	Ala	Asp	
240					245				250					255		
GAA	GAC	CAT	TAC	CGG	GAG	CAA	CAG	GCT	CTG	AAT	GAA	AGT	ACC	ACC	AAA	936
Glu	Asp	His	Tyr	Arg	Glu	Gln	Gln	Ala	Leu	Asn	Glu	Ser	Thr	Thr	Lys	
				260				265						270		
AAT	GGA	GCT	GCC	AGC	AAA	CGT	GCA	TTC	AAG	CAG	AGC	CCC	CCT	GCC	ATC	984
Asn	Gly	Ala	Ala	Ser	Lys	Arg	Ala	Phe	Lys	Gln	Ser	Pro	Pro	Ala	Ile	
			275				280						285			
CCT	GCC	CTG	GGT	ACC	AAC	GTG	AAG	AAG	AGA	CGC	CAC	GGG	GAC	GAG	GAC	1032
Pro	Ala	Leu	Gly	Thr	Asn	Val	Lys	Lys	Arg	Arg	His	Gly	Asp	Glu	Asp	
		290					295					300				
ATG	TTC	TAC	ATG	CAC	GTG	CGA	GGC	CGG	GAG	AAC	TTT	GAG	ATC	TTG	ATG	1080
Met	Phe	Tyr	Met	His	Val	Arg	Gly	Arg	Glu	Asn	Phe	Glu	Ile	Leu	Met	
	305					310					315					
AAA	GTC	AAG	GAG	AGC	CTA	GAA	CTG	ATG	GAG	CTT	GTG	CCC	CAG	CCT	TTG	1128
Lys	Val	Lys	Glu	Ser	Leu	Glu	Leu	Met	Glu	Leu	Val	Pro	Gln	Pro	Leu	

AS  
W

320	325	330	335	
GTT GAC TCC TAT CGA CAG CAG CAG CAG CAG CAG CTC CTA CAG AGG CCG				1176
Val Asp Ser Tyr Arg Gln Gln Gln Gln Gln Gln Leu Leu Gln Arg Pro	340	345	350	
AGT CAC CTG CAG CCT CCA TCC TAT GGG CCC GTG CTC TCC CCA ATG AAC				1224
Ser His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn	355	360	365	
AAG GTA CAC GGT GGT GTC AAC AAA CTG CCC TCC GTC AAC CAG CTG GTG				1272
Lys Val His Gly Gly Val Asn Lys Leu Pro Ser Val Asn Gln Leu Val	370	375	380	
GGC CAG CCT CCC CCG CAC AGC TCA GCA GCT GGG CCC AAC CTG GGG CCC				1320
Gly Gln Pro Pro Pro His Ser Ser Ala Ala Gly Pro Asn Leu Gly Pro	385	390	395	
ATG GGC TCC GGG ATG CTC AAC AGC CAC GGC CAC AGC ATG CCG GCC AAT				1368
Met Gly Ser Gly Met Leu Asn Ser His Gly His Ser Met Pro Ala Asn	400	405	410	415
GGT GAG ATG AAT GGA GGC CAC AGC TCC CAG ACC ATG GTT TCG GGA TCC				1416
Gly Glu Met Asn Gly Gly His Ser Ser Gln Thr Met Val Ser Gly Ser	420	425	430	
CAC TGC ACC CCG CCA CCC CCC TAT CAT GCA GAC CCC AGC CTC GTC AGT				1464
His Cys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser	435	440	445	
TTT TTG ACA GGG TTG GGG TGT CCA AAC TGC ATC GAG TGC TTC ACT TCC				1512
Phe Leu Thr Gly Leu Gly Cys Pro Asn Cys Ile Glu Cys Phe Thr Ser	450	455	460	
CAA GGG TTG CAG AGC ATC TAC CAC CTG CAG AAC CTT ACC ATC GAG GAC				1560
Gln Gly Leu Gln Ser Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp	465	470	475	
CTT GGG GCT CTG AAG GTC CCT GAC CAG TAC CGT ATG ACC ATC TGG AGG				1608
Leu Gly Ala Leu Lys Val Pro Asp Gln Tyr Arg Met Thr Ile Trp Arg	480	485	490	495
GGC CTA CAG GAC CTG AAG CAG AGC CAT GAC TGC GGC CAG CAA CTG CTA				1656
Gly Leu Gln Asp Leu Lys Gln Ser His Asp Cys Gly Gln Gln Leu Leu	500	505	510	
CGC TCC AGC AGC AAC GCG GCC ACC ATC TCC ATC GGC GGC TCT GGC GAG				1704
Arg Ser Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu	515	520	525	
CTG CAG CGG CAG CGG GTC ATG GAA GCC GTG CAT TTC CGT GTG CGC CAC				1752
Leu Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His	530	535	540	
ACC ATC ACA ATC CCC AAC CGT GGA GGC GCA GGT GCG GTG ACA GGT CCC				1800
Thr Ile Thr Ile Pro Asn Arg Gly Gly Ala Gly Ala Val Thr Gly Pro	545	550	555	

AS  
WI

GAC GAG TGG GCG GAC TTT GGC TTT GAC CTG CCT GAC TGC AAG TCC CGT 1848  
 Asp Glu Trp Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ser Arg  
 560 565 570 575

AAG CAG CCC ATC AAA GAG GAG TTC ACA GAG ACA GAG AGC CAC 1890  
 Lys Gln Pro Ile Lys Glu Glu Phe Thr Glu Thr Glu Ser His  
 580 585

TGAGGAACGT ACCTTCTTCT CCTGTCCTTC CTCTGTGAGA AACTGCTCTT GGAAGTGGGA 1950

CCTGTTGGCT GTGCCCACAG AAACCAGCAA GGACCTTCTG CCGGATGCCA TTCCTGAAGG 2010

GAAGTCGCTC ATGAACCTAAC TCCCTCTTGG 2040

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<212> PRT

<213> Mus musculus

<400> 8

Met Cys Met Gly Pro Val Tyr Glu Ser Leu Gly Gln Ala Gln Phe Asn  
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Leu Leu Ser Ser Ala Met Asp Gln Met Gly Ser Arg Ala Ala Pro Ala  
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Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Ala Pro Thr His Ser Pro  
 35 40 45

*AS*  
 Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro Val  
 50 55 60

Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu Val Thr  
 65 70 75 80

Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Pro  
 85 90 95

Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln  
 100 105 110

Ile Lys Val Ser Thr Pro Pro Pro Gly Thr Ala Ile Arg Ala Met  
 115 120 125

Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Ile Val Lys Arg Cys  
 130 135 140

Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser Ala Pro  
 145 150 155 160

Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ala Gln Tyr Val  
 165 170 175

Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr Glu Pro  
 180 185 190

Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe Met Cys  
 195 200 205

Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Val Ile  
 210 215 220

Ile Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Ser Phe  
 225 230 235 240

Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu  
 245 250 255

Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Thr Thr Lys Asn  
 260 265 270

Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala Ile Pro  
 275 280 285

Ala Leu Gly Thr Asn Val Lys Lys Arg Arg His Gly Asp Glu Asp Met  
 290 295 300

Phe Tyr Met His Val Arg Gly Arg Glu Asn Phe Glu Ile Leu Met Lys  
 305 310 315 320

Val Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro Leu Val  
 325 330 335

Asp Ser Tyr Arg Gln Gln Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser  
 340 345 350

His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys  
 355 360 365

Val His Gly Gly Val Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly  
 370 375 380

Gln Pro Pro Pro His Ser Ser Ala Ala Gly Pro Asn Leu Gly Pro Met  
 385 390 395 400

Gly Ser Gly Met Leu Asn Ser His Gly His Ser Met Pro Ala Asn Gly  
 405 410 415

Glu Met Asn Gly Gly His Ser Ser Gln Thr Met Val Ser Gly Ser His  
 420 425 430

Cys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe  
 435 440 445

Leu Thr Gly Leu Gly Cys Pro Asn Cys Ile Glu Cys Phe Thr Ser Gln  
 450 455 460

Gly Leu Gln Ser Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp Leu  
 465 470 475 480

Gly Ala Leu Lys Val Pro Asp Gln Tyr Arg Met Thr Ile Trp Arg Gly  
485 490 495

Leu Gln Asp Leu Lys Gln Ser His Asp Cys Gly Gln Gln Leu Leu Arg  
500 505 510

Ser Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu Leu  
515 520 525

Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His Thr  
530 535 540

Ile Thr Ile Pro Asn Arg Gly Gly Ala Gly Ala Val Thr Gly Pro Asp  
545 550 555 560

Glu Trp Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ser Arg Lys  
565 570 575

Gln Pro Ile Lys Glu Glu Phe Thr Glu Thr Glu Ser His  
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<222> 389..757

<400> 9

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GGGCCCCGAGA CCCCAGACTCG GGCAGAGCCA GCTGGGGAGG CGGGGCGCGC GTGGGAGCCA 180  
GGGGCCCCGGG TGGCCGGCCC TCCTCCGCCA CGGCTGAGTG CCCGCGCTGC CTTCCCGCCG 240  
GTCCGCCAAG AAAGGCGCTA AGCCTGCGGC AGTCCCCTCG CCGCCGCCTC CCTGCTCCGC 300  
ACCCTTATAA CCCGCCGTCC CGCATCCAGG CGAGGAGGCA ACGCTGCAGC CCAGCCCTCG 360  
CCGACGCCGA CGCCCGGCCC GGAGCAGA ATG AGC GGC AGC GTT GGG GAG ATG 412  
Met Ser Gly Ser Val Gly Glu Met  
1 5  
GCC CAG ACC TCT TCT TCC TCC TCC TCC ACC TTC GAG CAC CTG TGG AGT 460  
Ala Gln Thr Ser Ser Ser Ser Ser Ser Thr Phe Glu His Leu Trp Ser  
10 15 20  
TCT CTA GAG CCA GAC AGC ACC TAC TTT GAC CTC CCC CAG CCC AGC CAA 508  
Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro Gln Pro Ser Gln  
25 30 35 40  
GGG ACT AGC GAG GCA TCA GGC AGC GAG GAG TCC AAC ATG GAT GTC TTC 556

Gly Thr Ser Glu Ala Ser Gly Ser Glu Glu Ser Asn Met Asp Val Phe  
 45 50 55

CAC CTG CAA GGC ATG GCC CAG TTC AAT TTG CTC AGC AGT GCC ATG GAC 604  
 His Leu Gln Gly Met Ala Gln Phe Asn Leu Leu Ser Ser Ala Met Asp  
 60 65 70

CAG ATG GGC AGC CGT GCG GCC CCG GCG AGC CCC TAC ACC CCG GAG CAC 652  
 Gln Met Gly Ser Arg Ala Ala Pro Ala Ser Pro Tyr Thr Pro Glu His  
 75 80 85

GCC GCC AGC GCG CCC ACC CAC TCG CCC TAC GCG CAG CCC AGC TCC ACC 700  
 Ala Ala Ser Ala Pro Thr His Ser Pro Tyr Ala Gln Pro Ser Ser Thr  
 90 95 100

TTC GAC ACC ATG TCT CCG GCG CCT GTC ATC CCT TCC AAT ACC GAC TAC 748  
 Phe Asp Thr Met Ser Pro Ala Pro Val Ile Pro Ser Asn Thr Asp Tyr  
 105 110 115 120

CCC GGC CCC C 758  
 Pro Gly Pro

<210> 10  
 <211> 123  
 <212> PRT  
 <213> Mus musculus

<400> 10

Met Ser Gly Ser Val Gly Glu Met Ala Gln Thr Ser Ser Ser Ser Ser  
 1 5 10 15

Ser Thr Phe Glu His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr  
 20 25 30

Phe Asp Leu Pro Gln Pro Ser Gln Gly Thr Ser Glu Ala Ser Gly Ser  
 35 40 45

Glu Glu Ser Asn Met Asp Val Phe His Leu Gln Gly Met Ala Gln Phe  
 50 55 60

Asn Leu Leu Ser Ser Ala Met Asp Gln Met Gly Ser Arg Ala Ala Pro  
 65 70 75 80

Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Ala Pro Thr His Ser  
 85 90 95

Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro  
 100 105 110

Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro  
 115 120

AS  
 W

<210> 11  
 <211> 559  
 <212> DNA  
 <213> Homo sapiens

<400> 11

CGACCTTCCC CAGTCAAGCC GGGGGAATAA TGAGGTGGTG GCGGAACGG ATTCCAGCAT	60
GGACGTCTTC CACCTGGAGG GCATGACTAC ATCTGTCATG CATCCTCGGC TCCTGCCTCA	120
CTAGCTGCGG AGCCTCTCCC GCTCGGTCCA CGCTGCCGGG CGGCCACGAC CGTGACCCTT	180
CCCCTCGGGC CGCCCAGATC CATGCCTCGT CCCACGGGAC ACCAGTTCCC TGGCGTGTGC	240
AGACCCCCCG GCGCCTACCA TGCTGTACGT CGGTGACCCC GCACGGCACC TCGCCACGGC	300
CCAGTTCAAT CTGCTGAGCA GCACCATGGA CCAGATGAGC AGCCGCGCGG CCTCGGCCAG	360
CCCCTACACC CCAGAGCACG CCGCCAGCGT GCCCACCAC TCGCCCTACG CACAACCCAG	420
CTCCACCTTC GACACCATGT CGCCGGCGCC TGTCATCCCC TCCAACACCG ACTACCCCGG	480
ACCCACCAC TTTGAGGTCA CTTTCCAGCA GTCCAGCACG GCCAAGTCAG CCACCTGGAC	540
GTACTCCCCG CTCTTGAAG	559

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 <211> 1764  
 <212> DNA  
 <213> Homo sapiens

<400> 12

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AGCACCATGG ACCAGATGAG CAGCCGCGCG GCCTCGGCCA GCCCCTACAC CCCAGAGCAC	120
GCCGCCAGCG TGCCCACCCA CTCGCCCTAC GCACAACCCA GCTCCACCTT CGACACCATG	180
TCGCCGGCGC CTGTCATCCC CTCCAACACC GACTACCCCG GACCCACCA CTTTGAGGTC	240
ACTTTCCAGC AGTCCAGCAC GGCCAAGTCA GCCACCTGGA CGTACTCCCC GCTCTTGAAG	300
AAACTCTACT GCCAGATCGC CAAGACATGC CCCATCCAGA TCAAGGTGTC CACCCCGCCA	360
CCCCCAGGCA CTGCCATCCG GGCCATGCCT GTTTACAAGA AAGCGGAGCA CGTGACCGAC	420
GTCGTGAAAC GCTGCCCCAA CCACGAGCTC GGGAGGGACT TCAACGAAGG ACAGTCTGCT	480
CCAGCCAGCC ACCTCATCCG CGTGGAAGGC AATAATCTCT CGCAGTATGT GGATGACCCT	540
GTCACCGGCA GGCAGAGCGT CGTGGTGCCC TATGAGCCAC CACAGGTGGG GACGGAATTC	600
ACCACCATCC TGTACAACTT CATGTGTAAC AGCAGCTGTG TAGGGGGCAT GAACCGGCGG	660



CCCATCCTCA TCATCATCAC CCTGGAGATG CGGGATGGGC AGGTGCTGGG CCGCCGGTCC 720  
 TTTGAGGGCC GCATCTGCGC CTGTCTTGGC CGCGACCGAA AAGCTGATGA GGACCACTAC 780  
 CGGGAGCAGC AGGCCCTGAA CGAGAGCTCC GCCAAGAACG GGGCCGCCAG CAAGCGTGCC 840  
 TTCAAGCAGA GCCCCCTGC CGTCCCCGCC CTTGGTGCCG GTGTGAAGAA GCGGCGGCAT 900  
 GGAGACGAGG ACACGTACTA CCTTCAGGTG CGAGGCCGGG AGAACTTTGA GATCCTGATG 960  
 AAGCTGAAAG AGAGCCTGGA GCTGATGGAG TTGGTGCCGC AGCCACTGGT GGACTCCTAT 1020  
 CGGCAGCAGC AGCAGCTCCT ACAGAGGCCG AGTCACCTAC AGCCCCCGTC CTACGGGCGG 1080  
 GTCTCTCTGC CCATGAACAA GGTGCACGGG GGCATGAACA AGCTGCCCTC CGTCAACCAG 1140  
 CTGGTGGGCC AGCCTCCCCC GCACAGTTTC GCAGCTACAC CCAACCTGGG GCGCGTGGGC 1200  
 CCCGGGATGC TCAACAACCA TGGCCACGCA GTGCCAGCCA ACGGCGAGAT GAGCAGCAGC 1260  
 CACAGCGCCC AGTCCATGGT CTCGGGGTCC CACTGCACTC CGCCACCCCC CTACCACGCC 1320  
 GACCCAGCC TCGTCAGTTT TTTAACAGGA TTGGGGTGTC CAAACTGCAT CGAGTATTTT 1380  
 ACCTCCAAG GGTACAGAG CATTTACCAC CTGCAGAACC TGACCATTGA GGACCTGGGG 1440  
 GCCCTGAAGA TCCCCGAGCA GTACCGCATG ACCATCTGGC GGGGCCTGCA GGACCTGAAG 1500  
 CAGGGCCACG ACTACAGCAC CGCGCAGCAG CTGCTCCGCT CTAGCAACGC GGCCACCATC 1560  
 TCCATCGGCG GCTCAGGGGA ACTGCAGCGC CAGCGGGTCA TGGAGGCCGT GCACTTCCGC 1620  
 GTGCGCCACA CCATCACCAT CCCCACCGC GCGGGCCAG GCGGCGGCC TGACGAGTGG 1680  
 GCGGACTTCG GCTTCGACCT GCCCGACTGC AAGGCCCGCA AGCAGCCCAT CAAGGAGGAG 1740  
 TTCACGGAGG CCGAGATCCA CTGA 1764

<210> 13  
 <211> 587  
 <212> PRT  
 <213> Homo sapiens

<400> 13

Met Leu Tyr Val Gly Asp Pro Ala Arg His Leu Ala Thr Ala Gln Phe  
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 Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala Ser  
 20 25 30  
 Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His Ser  
 35 40 45  
 Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro  
 50 55 60

Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu Val  
 65 70 75 80  
 Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser  
 85 90 95  
 Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile  
 100 105 110  
 Gln Ile Lys Val Ser Thr Pro Pro Pro Pro Gly Thr Ala Ile Arg Ala  
 115 120 125  
 Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys Arg  
 130 135 140  
 Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser Ala  
 145 150 155 160  
 Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln Tyr  
 165 170 175  
 Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr Glu  
 180 185 190  
 Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe Met  
 195 200 205  
 Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile  
 210 215 220  
 Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg Ser  
 225 230 235 240  
 Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp  
 245 250 255  
 Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala Lys  
 260 265 270  
 Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala Val  
 275 280 285  
 Pro Ala Leu Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu Asp  
 290 295 300  
 Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu Met  
 305 310 315 320  
 Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro Leu  
 325 330 335  
 Val Asp Ser Tyr Arg Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser His  
 340 345 350  
 Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys Val  
 355 360 365

AS  
WT

His Gly Gly Met Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly Gln  
370 375 380

Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val Gly  
385 390 395 400

Pro Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Gly Glu  
405 410 415

Met Ser Ser Ser His Ser Ala Gln Ser Met Val Ser Gly Ser His Cys  
420 425 430

Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe Leu  
435 440 445

Thr Gly Leu Gly Cys Pro Asn Cys Ile Glu Tyr Phe Thr Ser Gln Gly  
450 455 460

Leu Gln Ser Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp Leu Gly  
465 470 475 480

Ala Leu Lys Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly Leu  
485 490 495

Gln Asp Leu Lys Gln Gly His Asp Tyr Ser Thr Ala Gln Gln Leu Leu  
500 505 510

Arg Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu Leu  
515 520 525

Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His Thr  
530 535 540

Ile Thr Ile Pro Asn Arg Gly Gly Pro Gly Gly Gly Pro Asp Glu Trp  
545 550 555 560

Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys Gln Pro  
565 570 575

Ile Lys Glu Glu Phe Thr Glu Ala Glu Ile His  
580 585

<210> 14

<211> 1521

<212> DNA

<213> Homo sapiens

<400> 14

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GCCGCCAGCG TGCCCACCCA CTCGCCCTAC GCACAACCCA GCTCCACCTT CGACACCATG 180

TCGCCGGCGC CTGTCATCCC CTCCAACACC GACTACCCCG GACCCACCA CTTTGAGGTC 240  
 ACTTTCCAGC AGTCCAGCAC GGCCAAGTCA GCCACCTGGA CGTACTCCCC GCTCTTGAAG 300  
 AAACCTCTACT GCCAGATCGC CAAGACATGC CCCATCCAGA TCAAGGTGTC CACCCCGCCA 360  
 CCCCCAGGCA CTGCCATCCG GGCCATGCCT GTTTACAAGA AAGCGGAGCA CGTGACCGAC 420  
 GTCGTGAAAC GCTGCCCCAA CCACGAGCTC GGGAGGGACT TCAACGAAGG ACAGTCTGCT 480  
 CCAGCCAGCC ACCTCATCCG CGTGGAAGGC AATAATCTCT CGCAGTATGT GGATGACCCCT 540  
 GTCACCGGCA GGCAGAGCGT CGTGGTGCCC TATGAGCCAC CACAGGTGGG GACGGAATTC 600  
 ACCACCATCC TGTACAACTT CATGTGTAAC AGCAGCTGTG TAGGGGGCAT GAACCGGCGG 660  
 CCCATCCTCA TCATCATCAC CCTGGAGATG CGGGATGGGC AGGTGCTGGG CCGCCGGTCC 720  
 TTTGAGGGCC GCATCTGCGC CTGTCCTGGC CGCGACCGAA AAGCTGATGA GGACCACTAC 780  
 CGGGAGCAGC AGGCCCTGAA CGAGAGCTCC GCCAAGAACG GGGCCGCCAG CAAGCGTGCC 840  
 TTCAAGCAGA GCCCCCTGC CGTCCCCGCC CTTGGTGCCG GTGTGAAGAA GCGGCGGCAT 900  
 GGAGACGAGG ACACGTACTA CCTTCAGGTG CGAGGCCGGG AGAACTTTGA GATCCTGATG 960  
 AAGCTGAAAG AGAGCCTGGA GCTGATGGAG TTGGTGCCGC AGCCACTGGT GGACTCCTAT 1020  
 CGGCAGCAGC AGCAGCTCCT ACAGAGGCCG CCCCAGGATG CTCAACAACC ATGGCCACGC 1080  
 AGTGCCAGCC AACGGCGAGA TGAGCAGCAG CCACAGCGCC CAGTCCATGG TCTCGGGGTC 1140  
 CCACTGCACT CCGCCACCCC CCTACCACGC CGACCCACAG CTCGTCAGGA CCTGGGGGCC 1200  
 CTGAAGATCC CCGAGCAGTA CCGCATGACC ATCTGGCGGG GCCTGCAGGA CCTGAAGCAG 1260  
 GGCCACGACT ACAGCACCGC GCAGCAGCTG CTCCGCTCTA GCAACGCGGC CACCATCTCC 1320  
 ATCGGCGGCT CAGGGGAACT GCAGCGCCAG CGGGTCATGG AGGCCGTGCA CTTCCGCGTG 1380  
 CGCCACACCA TCACCATCCC CAACCGCGGC GGCCCAGGCG GCGGCCCTGA CGAGTGGGCG 1440  
 GACTTCGGCT TCGACCTGCC CGACTGCAAG GCCCGCAAGC AGCCCATCAA GGAGGAGTTC 1500  
 ACGGAGGCCG AGATCCACTG A 1521

&lt;210&gt; 15

&lt;211&gt; 506

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 15

Met Leu Tyr Val Gly Asp Pro Ala Arg His Leu Ala Thr Ala Gln Phe  
 1 5 10 15

Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala Ser  
 20 25 30  
 Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His Ser  
 35 40 45  
 Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro  
 50 55 60  
 Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu Val  
 65 70 75 80  
 Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser  
 85 90 95  
 Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile  
 100 105 110  
 Gln Ile Lys Val Ser Thr Pro Pro Pro Pro Gly Thr Ala Ile Arg Ala  
 115 120 125  
 Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys Arg  
 130 135 140  
 Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser Ala  
 145 150 155 160  
 Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln Tyr  
 165 170 175  
 Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr Glu  
 180 185 190  
 Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe Met  
 195 200 205  
 Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile  
 210 215 220  
 Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg Ser  
 225 230 235 240  
 Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp  
 245 250 255  
 Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala Lys  
 260 265 270  
 Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala Val  
 275 280 285  
 Pro Ala Leu Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu Asp  
 290 295 300  
 Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu Met  
 305 310 315 320

AS

30

Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro Leu  
 325 330 335

Val Asp Ser Tyr Arg Gln Gln Gln Gln Leu Leu Gln Arg Pro Pro Arg  
 340 345 350

Asp Ala Gln Gln Pro Trp Pro Arg Ser Ala Ser Gln Arg Arg Asp Glu  
 355 360 365

Gln Gln Pro Gln Arg Pro Val His Gly Leu Gly Val Pro Leu His Ser  
 370 375 380

Ala Thr Pro Leu Pro Arg Arg Pro Gln Pro Arg Gln Asp Leu Gly Ala  
 385 390 395 400

Leu Lys Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly Leu Gln  
 405 410 415

Asp Leu Lys Gln Gly His Asp Tyr Ser Thr Ala Gln Gln Leu Leu Arg  
 420 425 430

Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu Leu Gln  
 435 440 445

Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His Thr Ile  
 450 455 460

Thr Ile Pro Asn Arg Gly Gly Pro Gly Gly Gly Pro Asp Glu Trp Ala  
 465 470 475 480

Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys Gln Pro Ile  
 485 490 495

Lys Glu Glu Phe Thr Glu Ala Glu Ile His  
 500 505

AS  
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<210> 16  
 <211> 1870  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> 104..1867

<400> 16

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AAGCCGGGGG AATAATGAGG TGGTGGGCGG AACGGATTCC AGC ATG GAC GTC TTC 115  
 Met Asp Val Phe  
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CAC CTG GAG GGC ATG ACT ACA TCT GTC ATG GCC CAG TTC AAT CTG CTG 163  
 His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln Phe Asn Leu Leu  
 5 10 15 20

AGC AGC ACC ATG GAC CAG ATG AGC AGC CGC GCG GCC TCG GCC AGC CCC 211

Ser	Ser	Thr	Met	Asp	Gln	Met	Ser	Ser	Arg	Ala	Ala	Ser	Ala	Ser	Pro	
				25					30						35	
TAC	ACC	CCA	GAG	CAC	GCC	GCC	AGC	GTG	CCC	ACC	CAC	TCG	CCC	TAC	GCA	259
Tyr	Thr	Pro	Glu	His	Ala	Ala	Ser	Val	Pro	Thr	His	Ser	Pro	Tyr	Ala	
			40					45					50			
CAA	CCC	AGC	TCC	ACC	TTC	GAC	ACC	ATG	TCG	CCG	GCG	CCT	GTC	ATC	CCC	307
Gln	Pro	Ser	Ser	Thr	Phe	Asp	Thr	Met	Ser	Pro	Ala	Pro	Val	Ile	Pro	
		55					60					65				
TCC	AAC	ACC	GAC	TAC	CCC	GGA	CCC	CAC	CAC	TTT	GAG	GTC	ACT	TTC	CAG	355
Ser	Asn	Thr	Asp	Tyr	Pro	Gly	Pro	His	His	Phe	Glu	Val	Thr	Phe	Gln	
	70					75					80					
CAG	TCC	AGC	ACG	GCC	AAG	TCA	GCC	ACC	TGG	ACG	TAC	TCC	CCG	CTC	TTG	403
Gln	Ser	Ser	Thr	Ala	Lys	Ser	Ala	Thr	Trp	Thr	Tyr	Ser	Pro	Leu	Leu	
	85				90				95						100	
AAG	AAA	CTC	TAC	TGC	CAG	ATC	GCC	AAG	ACA	TGC	CCC	ATC	CAG	ATC	AAG	451
Lys	Lys	Leu	Tyr	Cys	Gln	Ile	Ala	Lys	Thr	Cys	Pro	Ile	Gln	Ile	Lys	
				105				110						115		
GTG	TCC	ACC	CCG	CCA	CCC	CCA	GGC	ACT	GCC	ATC	CGG	GCC	ATG	CCT	GTT	499
Val	Ser	Thr	Pro	Pro	Pro	Pro	Gly	Thr	Ala	Ile	Arg	Ala	Met	Pro	Val	
			120				125						130			
TAC	AAG	AAA	GCG	GAG	CAC	GTG	ACC	GAC	GTC	GTG	AAA	CGC	TGC	CCC	AAC	547
Tyr	Lys	Lys	Ala	Glu	His	Val	Thr	Asp	Val	Val	Lys	Arg	Cys	Pro	Asn	
			135				140					145				
CAC	GAG	CTC	GGG	AGG	GAC	TTC	AAC	GAA	GGA	CAG	TCT	GCT	CCA	GCC	AGC	595
His	Glu	Leu	Gly	Arg	Asp	Phe	Asn	Glu	Gly	Gln	Ser	Ala	Pro	Ala	Ser	
	150					155					160					
CAC	CTC	ATC	CGC	GTG	GAA	GGC	AAT	AAT	CTC	TCG	CAG	TAT	GTG	GAT	GAC	643
His	Leu	Ile	Arg	Val	Glu	Gly	Asn	Asn	Leu	Ser	Gln	Tyr	Val	Asp	Asp	
	165				170				175					180		
CCT	GTC	ACC	GGC	AGG	CAG	AGC	GTC	GTG	GTG	CCC	TAT	GAG	CCA	CCA	CAG	691
Pro	Val	Thr	Gly	Arg	Gln	Ser	Val	Val	Val	Pro	Tyr	Glu	Pro	Pro	Gln	
				185				190						195		
GTG	GGG	ACG	GAA	TTC	ACC	ACC	ATC	CTG	TAC	AAC	TTC	ATG	TGT	AAC	AGC	739
Val	Gly	Thr	Glu	Phe	Thr	Thr	Ile	Leu	Tyr	Asn	Phe	Met	Cys	Asn	Ser	
			200				205						210			
AGC	TGT	GTA	GGG	GGC	ATG	AAC	CGG	CGG	CCC	ATC	CTC	ATC	ATC	ATC	ACC	787
Ser	Cys	Val	Gly	Gly	Met	Asn	Arg	Arg	Pro	Ile	Leu	Ile	Ile	Ile	Thr	
			215				220					225				
CTG	GAG	ATG	CGG	GAT	GGG	CAG	GTG	CTG	GGC	CGC	CGG	TCC	TTT	GAG	GGC	835
Leu	Glu	Met	Arg	Asp	Gly	Gln	Val	Leu	Gly	Arg	Arg	Ser	Phe	Glu	Gly	
	230					235					240					
CGC	ATC	TGC	GCC	TGT	CCT	GGC	CGC	GAC	CGA	AAA	GCT	GAT	GAG	GAC	CAC	883
Arg	Ile	Cys	Ala	Cys	Pro	Gly	Arg	Asp	Arg	Lys	Ala	Asp	Glu	Asp	His	

AS  
Ed

245	250	255	260	
TAC CGG GAG CAG CAG GCC CTG AAC GAG AGC TCC GCC AAG AAC GGG GCC				931
Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala Lys Asn Gly Ala	265	270	275	
GCC AGC AAG CGT GCC TTC AAG CAG AGC CCC CCT GCC GTC CCC GCC CTT				979
Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala Val Pro Ala Leu	280	285	290	
GGT GCC GGT GTG AAG AAG CGG CGG CAT GGA GAC GAG GAC ACG TAC TAC				1027
Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu Asp Thr Tyr Tyr	295	300	305	
CTT CAG GTG CGA GGC CGG GAG AAC TTT GAG ATC CTG ATG AAG CTG AAA				1075
Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu Met Lys Leu Lys	310	315	320	
GAG AGC CTG GAG CTG ATG GAG TTG GTG CCG CAG CCA CTG GTG GAC TCC				1123
Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro Leu Val Asp Ser	325	330	335	340
TAT CGG CAG CAG CAG CAG CTC CTA CAG AGG CCG AGT CAC CTA CAG CCC				1171
Tyr Arg Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser His Leu Gln Pro	345	350	355	
CCG TCC TAC GGG CCG GTC CTC TCG CCC ATG AAC AAG GTG CAC GGG GGC				1219
Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys Val His Gly Gly	360	365	370	
ATG AAC AAG CTG CCC TCC GTC AAC CAG CTG GTG GGC CAG CCT CCC CCG				1267
Met Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly Gln Pro Pro Pro	375	380	385	
CAC AGT TCG GCA GCT ACA CCC AAC CTG GGG CCC GTG GGC CCC GGG ATG				1315
His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val Gly Pro Gly Met	390	395	400	
CTC AAC AAC CAT GGC CAC GCA GTG CCA GCC AAC GGC GAG ATG AGC AGC				1363
Leu Asn Asn His Gly His Ala Val Pro Ala Asn Gly Glu Met Ser Ser	405	410	415	420
AGC CAC AGC GCC CAG TCC ATG GTC TCG GGG TCC CAC TGC ACT CCG CCA				1411
Ser His Ser Ala Gln Ser Met Val Ser Gly Ser His Cys Thr Pro Pro	425	430	435	
CCC CCC TAC CAC GCC GAC CCC AGC CTC GTC AGT TTT TTA ACA GGA TTG				1459
Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe Leu Thr Gly Leu	440	445	450	
GGG TGT CCA AAC TGC ATC GAG TAT TTC ACC TCC CAA GGG TTA CAG AGC				1507
Gly Cys Pro Asn Cys Ile Glu Tyr Phe Thr Ser Gln Gly Leu Gln Ser	455	460	465	
ATT TAC CAC CTG CAG AAC CTG ACC ATT GAG GAC CTG GGG GCC CTG AAG				1555
Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp Leu Gly Ala Leu Lys	470	475	480	

AS  
ent



ATC CCC GAG CAG TAC CGC ATG ACC ATC TGG CGG GGC CTG CAG GAC CTG 1603  
 Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly Leu Gln Asp Leu  
 485 490 495 500

AAG CAG GGC CAC GAC TAC AGC ACC GCG CAG CAG CTG CTC CGC TCT AGC 1651  
 Lys Gln Gly His Asp Tyr Ser Thr Ala Gln Gln Leu Leu Arg Ser Ser  
 505 510 515

AAC GCG GCC ACC ATC TCC ATC GGC GGC TCA GGG GAA CTG CAG CGC CAG 1699  
 Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu Leu Gln Arg Gln  
 520 525 530

CGG GTC ATG GAG GCC GTG CAC TTC CGC GTG CGC CAC ACC ATC ACC ATC 1747  
 Arg Val Met Glu Ala Val His Phe Arg Val Arg His Thr Ile Thr Ile  
 535 540 545

CCC AAC CGC GGC GGC CCA GGC GGC GGC CCT GAC GAG TGG GCG GAC TTC 1795  
 Pro Asn Arg Gly Gly Pro Gly Gly Gly Pro Asp Glu Trp Ala Asp Phe  
 550 555 560

GGC TTC GAC CTG CCC GAC TGC AAG GCC CGC AAG CAG CCC ATC AAG GAG 1843  
 Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys Gln Pro Ile Lys Glu  
 565 570 575 580

GAG TTC ACG GAG GCC GAG ATC CAC TGA 1870  
 Glu Phe Thr Glu Ala Glu Ile His  
 585

<210> 17

<211> 588

<212> PRT

<213> Homo Sapiens

<400> 17

Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln  
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Phe Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala  
 20 25 30

Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His  
 35 40 45

Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala  
 50 55 60

Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu  
 65 70 75 80

Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr  
 85 90 95

Ser Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro  
 100 105 110

AF  
GK

Ile Gln Ile Lys Val Ser Thr Pro Pro Pro Pro Gly Thr Ala Ile Arg  
 115 120 125

Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys  
 130 135 140

Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser  
 145 150 155 160

Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln  
 165 170 175

Tyr Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr  
 180 185 190

Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe  
 195 200 205

Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu  
 210 215 220

Ile Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg  
 225 230 235 240

Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala  
 245 250 255

Asp Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala  
 260 265 270

Lys Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala  
 275 280 285

Val Pro Ala Leu Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu  
 290 295 300

Asp Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu  
 305 310 315 320

Met Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro  
 325 330 335

Leu Val Asp Ser Tyr Arg Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser  
 340 345 350

His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys  
 355 360 365

Val His Gly Gly Met Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly  
 370 375 380

Gln Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val  
 385 390 395 400

Gly Pro Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Gly  
 405 410 415

AS  
at

Glu Met Ser Ser Ser His Ser Ala Gln Ser Met Val Ser Gly Ser His  
420 425 430

Cys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe  
435 440 445

Leu Thr Gly Leu Gly Cys Pro Asn Cys Ile Glu Tyr Phe Thr Ser Gln  
450 455 460

Gly Leu Gln Ser Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp Leu  
465 470 475 480

Gly Ala Leu Lys Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly  
485 490 495

Leu Gln Asp Leu Lys Gln Gly His Asp Tyr Ser Thr Ala Gln Gln Leu  
500 505 510

Leu Arg Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu  
515 520 525

Leu Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His  
530 535 540

Thr Ile Thr Ile Pro Asn Arg Gly Gly Pro Gly Gly Gly Pro Asp Glu  
545 550 555 560

Trp Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys Gln  
565 570 575

Pro Ile Lys Glu Glu Phe Thr Glu Ala Glu Ile His  
580 585

<210> 18

<211> 1817

<212> DNA

<213> Homo sapiens

<400> 18

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TCTCTGGAAC CAGACAGCAC CTA CTTCTCGAC CTTCCCCAGT CAAGCCGGGG GAATAATGAG	120
GTGGTGGGCG GAACGGATTC CAGCATGGAC GTCTTCCACC TGGAGGGCAT GACTACATCT	180
GTCATGGCCC AGTTCAATCT GCTGAGCAGC ACCATGGACC AGATGAGCAG CCGCGCGGCC	240
TCGGCCAGCC CCTACACCCC AGAGCACGCC GCCAGCGTGC CCACCCACTC GCCCTACGCA	300
CAACCCAGCT CCACCTTCGA CACCATGTCT CCGGCGCCTG TCATCCCCTC CAACACCGAC	360
TACCCCGGAC CCCACCACTT TGAGGTCAC TCCAGCAGT CCAGCACGGC CAAGTCAGCC	420
ACCTGGACGT ACTCCCCGCT CTTGAAGAAA CTCTACTGCC AGATCGCCAA GACATGCCCC	480

ATCCAGATCA AGGTGTCCAC CCCGCCACCC CCAGGCACCTG CCATCCGGGC CATGCCTGTT 540  
 TACAAGAAAG CGGAGCACGT GACCGACGTC GTGAAACGCT GCCCCAACCA CGAGCTCGGG 600  
 AGGGACTTCA ACGAAGGACA GTCTGCTCCA GCCAGCCACC TCATCCGCGT GGAAGGCAAT 660  
 AATCTCTCGC AGTATGTGGA TGACCCTGTC ACCGGCAGGC AGAGCGTCGT GGTGCCCTAT 720  
 GAGCCACCAC AGGTGGGGAC GGAATTCACC ACCATCCTGT ACAACTTCAT GTGTAACAGC 780  
 AGCTGTGTAG GGGGCATGAA CCGGCGGCCC ATCCTCATCA TCATCACCTT GGAGATGCGG 840  
 GATGGGCAGG TGCTGGGCCG CCGGTCCTTT GAGGGCCGCA TCTGCGCCTG TCCTGGCCGC 900  
 GACCGAAAAG CTGATGAGGA CCACTACCGG GAGCAGCAGG CCCTGAACGA GAGCTCCGCC 960  
 AAGAACGGGG CCGCCAGCAA GCGTGCCTTC AAGCAGAGCC CCCCTGCCGT CCCC GCCCTT 1020  
 GGTGCCGGTG TGAAGAAGCG GCGGCATGGA GACGAGGACA CGTACTACCT TCAGGTGCGA 1080  
 GGCCGGGAGA ACTTTGAGAT CCTGATGAAG CTGAAAGAGA GCCTGGAGCT GATGGAGTTG 1140  
 GTGCCGCAGC CACTGGTGGA CTCCTATCGG CAGCAGCAGC AGCTCCTACA GAGGCCGAGT 1200  
 CACCTACAGC CCCCCTCCTA CGGGCCGGTC CTCTCGCCCA TGAACAAGGT GCACGGGGGC 1260  
 ATGAACAAGC TGCCCTCCGT CAACCAGCTG GTGGGCCAGC CTCCCCCGCA CAGTTCGGCA 1320  
 GCTACACCCA ACCTGGGGCC CGTGGGCCCC GGGATGCTCA ACAACCATGG CCACGCAGTG 1380  
 CCAGCCAACG GCGAGATGAG CAGCAGCCAC AGCGCCAGT CCATGGTCTC GGGGTCCCAC 1440  
 TGCACTCCGC CACCCCCCTA CCACGCCGAC CCCAGCCTCG TCAGGACCTG GGGGCCCTGA 1500  
 AGATCCCCGA GCAGTACCGC ATGACCATCT GCGGGGGCCT GCAGGACCTG AAGCAGGGCC 1560  
 ACGACTACAG CACCGCGCAG CAGCTGCTCC GCTCTAGCAA CGCGGCCACC ATCTCCATCG 1620  
 GCGGCTCAGG GGAAGTGCAG CGCCAGCGGG TCATGGAGGC CGTGCACTTC CGCGTGCGCC 1680  
 ACACCATCAC CATCCCCAAC CGCGGCGGCC CAGGCGGCGG CCCTGACGAG TGGGCGGACT 1740  
 TCGGCTTCGA CCTGCCCCGAC TGCAAGGCCC GCAAGCAGCC CATCAAGGAG GAGTTCACGG 1800  
 AGGCCGAGAT CCACTGA 1817

<210> 19  
 <211> 499  
 <212> PRT  
 <213> Homo sapiens

<400> 19

Met Ala Gln Ser Thr Ala Thr Ser Pro Asp Gly Gly Thr Thr Phe Glu  
 1 5 10 15

His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro  
 20 25 30  
 Gln Ser Ser Arg Gly Asn Asn Glu Val Val Gly Gly Thr Asp Ser Ser  
 35 40 45  
 Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln  
 50 55 60  
 Phe Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala  
 65 70 75 80  
 Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His  
 85 90 95  
 Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala  
 100 105 110  
 Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu  
 115 120 125  
 Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr  
 130 135 140  
 Ser Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro  
 145 150 155 160  
 Ile Gln Ile Lys Val Ser Thr Pro Pro Pro Pro Gly Thr Ala Ile Arg  
 165 170 175  
 Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys  
 180 185 190  
 Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser  
 195 200 205  
 Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln  
 210 215 220  
 Tyr Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr  
 225 230 235 240  
 Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe  
 245 250 255  
 Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu  
 260 265 270  
 Ile Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg  
 275 280 285  
 Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala  
 290 295 300  
 Asp Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala  
 305 310 315 320

AST

38

Lys Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala  
325 330 335

Val Pro Ala Leu Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu  
340 345 350

Asp Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu  
355 360 365

Met Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro  
370 375 380

Leu Val Asp Ser Tyr Arg Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser  
385 390 395 400

His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys  
405 410 415

Val His Gly Gly Met Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly  
420 425 430

Gln Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val  
435 440 445

Gly Pro Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Gly  
450 455 460

Glu Met Ser Ser Ser His Ser Ala Gln Ser Met Val Ser Gly Ser His  
465 470 475 480

Cys Thr Pro Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Arg Thr  
485 490 495

Trp Gly Pro

<210> 20  
<211> 17  
<212> DNA  
<213> Artificial

<220>  
<223> primer

<400> 20

GCGAGCTGCC CTCGGAG

17

<210> 21  
<211> 19  
<212> DNA  
<213> Artificial

<220>  
<223> antisense primer

&lt;400&gt; 21

GGTTCTGCAG GTGACTCAG

19

&lt;210&gt; 22

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; primer

&lt;400&gt; 22

GCCATGCCTG TCTACAAG

18

&lt;210&gt; 23

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; antisense primer

&lt;400&gt; 23

ACCAGCTGGT TGACGGAG

18

AS

&lt;210&gt; 24

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; primer

&lt;400&gt; 24

GTCAACCAGC TGGTGGGCCA G

21

&lt;210&gt; 25

&lt;211&gt; 16

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; antisense primer

&lt;400&gt; 25

GTGGATCTCG GCCTCC

16

&lt;210&gt; 26

<211> 17  
 <212> DNA  
 <213> Artificial

<220>  
 <223> primer

<400> 26

AGGCCGGCGT GGGGAAG

17

<210> 27  
 <211> 19  
 <212> DNA  
 <213> Artificial

<220>  
 <223> antisense primer

<400> 27

CTTGGCGATC TGGCAGTAG

19

<210> 28  
 <211> 17  
 <212> DNA  
 <213> Artificial

<220>  
 <223> primer

<400> 28

GCGGCCACGA CCGTGAC

17

<210> 29  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
 <223> antisense primer

<400> 29

GGCAGCTTGG GTCTCTGG

18

<210> 30  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
 <223> primer

<400> 30

CTGTACGTCG GTGACCCC

18

AS  
 AS



<210> 31  
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 <212> DNA  
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<220>  
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<400> 31

TCAGTGGATC TCGGCCTC

18

<210> 32  
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 <212> DNA  
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<220>  
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<400> 32

AGGGGACGCA GCGAAACC

18

<210> 33  
 <211> 19  
 <212> DNA  
 <213> Artificial

<220>  
 <223> antisense primer

<400> 33

CCATCAGCTC CAGGCTCTC

19

<210> 34  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
 <223> antisense primer

<400> 34

CCAGGACAGG CGCAGATG

18

<210> 35  
 <211> 19  
 <212> DNA  
 <213> Artificial

<220>  
 <223> antisense primer

<400> 35

GATGAGGTGG CTGGCTGGA

19

<210> 36

<211> 19

<212> DNA

<213> Artificial

<220>

<223> antisense primer

<400> 36

TGGTCAGGTT CTGCAGGTG

19

<210> 37

<211> 18

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 37

CACCTACTCC AGGGATGC

18

<210> 38

<211> 21

<212> DNA

<213> Artificial

<220>

<223> antisense primer

<400> 38

AGGAAAATAG AAGCGTCAGT C

21

<210> 39

<211> 18

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 39

CAGGCCCACT TGCCTGCC

18

<210> 40

<211> 19

<212> DNA

<213> Artificial

<220>

<223> antisense primer

&lt;400&gt; 40

CTGTCCCCAA GCTGATGAG

19

&lt;210&gt; 41

&lt;211&gt; 15

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; primer

&lt;400&gt; 41

CCCCCCCCC CCCCD

15

&lt;210&gt; 42

&lt;211&gt; 16

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; primer

&lt;400&gt; 42

CCCCCCCCC CCCCCD

16

&lt;210&gt; 43

&lt;211&gt; 1400

&lt;212&gt; DNA

&lt;213&gt; Cebus apella

&lt;400&gt; 43

ggggctccgg ggacacttgg cgcccggggt ggaagcgtgc tttccaagac ggtgacacgc 60  
 ttccctgagg attggcagcc agactgctta cgggtcactg ccatggagga gccgcagtca 120  
 gatcccagca tcgagccccc tctgagtcag gaaacatttt cagacctatg gaaactactt 180  
 cctgaaaaca acgtttctgtc ccccttgccg tccaagcgg tggatgattt gatgctctct 240  
 ccggatgatc ttgcacaatg gttaactgaa gaccaggtc cagatgaagc tcccagaatg 300  
 tcagaggctg ctccccacat ggccccaca ccagcagctc ctacaccggc ggcccctgca 360  
 ccagccccct cctggccccct gtcactctct gtcccttccc agaaaacctt ccacggcagc 420  
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 cagcacatga ctgaggtcgt gaggcgctgc cccaccatg agcgtgctc agacagcgat 660  
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 gatgacagaa acacttttgc acatagtgtg gtggtgcctt atgagccgcc tgagggttggc 780  
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 gagaatttcc gcaagaaagg ggagccttgc cagcagctgc cccctgggag cactaagcga 1020  
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 tatttcaccc ttcagatccg cgggcgtgag cgcttcgaga tggtccgaga gctgaatgag 1140  
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cccccatctc tccctccctt gccattttga gttctggggtc tttaaaccct tgcttgcaat 1380  
 aggtgtgtgt cagaagcaaa 1400

<210> 44  
 <211> 393  
 <212> PRT  
 <213> Cebus apella

<400> 44

Met Glu Glu Pro Gln Ser Asp Pro Ser Ile Glu Pro Pro Leu Ser Gln  
 1 5 10 15

Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro Glu Asn Asn Val Leu  
 20 25 30

Ser Pro Leu Pro Ser Gln Ala Val Asp Asp Leu Met Leu Ser Pro Asp  
 35 40 45

Asp Leu Ala Gln Trp Leu Thr Glu Asp Pro Gly Pro Asp Glu Ala Pro  
 50 55 60

Arg Met Ser Glu Ala Ala Pro His Met Ala Pro Thr Pro Ala Ala Pro  
 65 70 75 80

Thr Pro Ala Ala Pro Ala Pro Ala Pro Ser Trp Pro Leu Ser Ser Ser  
 85 90 95

Val Pro Ser Gln Lys Thr Tyr His Gly Ser Tyr Gly Phe Arg Leu Gly  
 100 105 110

Phe Leu His Ser Gly Thr Ala Lys Ser Val Thr Cys Thr Tyr Ser Pro  
 115 120 125

Asp Leu Asn Lys Met Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln  
 130 135 140

Leu Trp Val Asp Ser Thr Pro Pro Pro Gly Ser Arg Val Arg Ala Met  
 145 150 155 160

Ala Ile Tyr Lys Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys  
 165 170 175

Pro His His Glu Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln  
 180 185 190

His Leu Ile Arg Val Glu Gly Asn Leu Arg Val Glu Tyr Ser Asp Asp  
 195 200 205

Arg Asn Thr Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu  
 210 215 220

Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn Ser  
 225 230 235 240

Ser Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr  
 245 250 255

Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val  
 260 265 270

Arg Val Cys Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn  
275 280 285

Phe Arg Lys Lys Gly Glu Pro Cys His Glu Leu Pro Pro Gly Ser Thr  
290 295 300

Lys Arg Ala Leu Pro Asn Asn Thr Ser Ser Ser Pro Gln Pro Lys Lys  
305 310 315 320

Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu  
325 330 335

Arg Phe Glu Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp  
340 345 350

Ala Gln Ala Gly Lys Glu Pro Ala Gly Ser Arg Ala His Ser Ser His  
355 360 365

Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys Phe Met  
370 375 380

Phe Lys Thr Glu Gly Pro Asp Ser Asp  
385 390

<210> 45

<211> 393

<212> PRT

<213> Homo sapiens

<400> 45

Met Glu Glu Pro Gln Ser Asp Pro Ser Val Glu Pro Pro Leu Ser Gln  
1 5 10 15

Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro Glu Asn Asn Val Leu  
20 25 30

Ser Pro Leu Pro Ser Gln Ala Met Asp Asp Leu Met Leu Ser Pro Asp  
35 40 45

Asp Ile Glu Gln Trp Phe Thr Glu Asp Pro Gly Pro Asp Glu Ala Pro  
50 55 60

Arg Met Pro Glu Ala Ala Pro Pro Val Ala Pro Ala Pro Ala Ala Pro  
65 70 75 80

Thr Pro Ala Ala Pro Ala Pro Ala Pro Ser Trp Pro Leu Ser Ser Ser  
85 90 95

Val Pro Ser Gln Lys Thr Tyr Gln Gly Ser Tyr Gly Phe Arg Leu Gly  
100 105 110

Phe Leu His Ser Gly Thr Ala Lys Ser Val Thr Cys Thr Tyr Ser Pro  
115 120 125

Ala Leu Asn Lys Met Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln  
130 135 140

Leu Trp Val Asp Ser Thr Pro Pro Pro Gly Thr Arg Val Arg Ala Met

AS  
44

46

145		150		155		160
Ala Ile Tyr Lys Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys						
	165			170		175
Pro His His Glu Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln						
	180		185		190	
His Leu Ile Arg Val Glu Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp						
	195		200		205	
Arg Asn Thr Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu						
	210		215		220	
Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn Ser						
	225		230		235	240
Ser Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr						
	245		250		255	
Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val						
	260		265		270	
Arg Val Cys Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn						
	275		280		285	
Leu Arg Lys Lys Gly Glu Pro His His Glu Leu Pro Pro Gly Ser Thr						
	290		295		300	
Lys Arg Ala Leu Pro Asn Asn Thr Ser Ser Ser Pro Gln Pro Lys Lys						
	305		310		315	320
Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu						
	325		330		335	
Arg Phe Glu Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp						
	340		345		350	
Ala Gln Gln Gly Lys Glu Pro Gly Gly Arg Ser Ala His Ser Ser His						
	355		360		365	
Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu Met						
	370		375		380	
Phe Lys Thr Glu Gly Pro Asp Ser Asp						
	385		390			

<210> 46  
 <211> 889  
 <212> DNA  
 <213> Homo sapiens

<400> 46  
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 gcgagctgcc ctcgagggcc ggcgtgggga agatggccca gtccaccgcc acctccccctg 180  
 atggggggcac cacgtttgag cactctgga gctctctgtg agtgcgcttg gctggccaga 240  
 gctggggggcc cccctgggag gcactctggg ctagcctcag ccaccttcgc tgggctaact 300  
 gggccagagc aggaggggtg gccccgggag gactctgggc tagccccagc caccctcact 360  
 gagactttgg gctaaacttg gcaaccctca ctgggattct gggctagcct cgaccaccct 420

tgctgcacta actggaccag agcaggagag gtggctccac actagtcttg ggctagcctt 480  
agccaccctc atcagcttgg ggacagggcg ggtcggaggg gcaggggaaga gggactgctg 540  
ccctaggcct tccctgggga tgcaggacca aaattcagac tcttttctct ggccagctct 600  
ggagagggcc catggccagc agaggcccag aataacagag cccatgactg gctctgcctc 660  
tctggcactc acagcagccc tggaatggca ggtggaggac agagatggga tgagagggaa 720  
tggaagggc aggagacgta ggcctcacca ggagtctcag gctagccttg agctctgggc 780  
ctgggaggtg ttgggggtgac acccaaactg gggactgacg cttctatttt cctctccctg 840  
ccccagggaa ccagacagca cctacttcga ccttccccag tcaagccgg 889

<210> 47

<211> 23

<212> DNA

<213> Artificial

<220>

<223> primer comprising BamHI site

<400> 47

gatccgggccc cttttttttt ttt 23

<210> 48

<211> 20

<212> DNA

<213> Artificial

<220>

<223> primer comprising ApaI site

<400> 48

aaaaaaaaaa aaagggcccg 20

<210> 49

<211> 26

<212> DNA

<213> Artificial

<220>

<223> primer comprising Kpn I site

<400> 49

actggtaccg cgagctgccc tcggag 26

<210> 50

<211> 28

<212> DNA

<213> Artificial

<220>

<223> antisense primer comprising Xba I site

<400> 50

gactctagag gttctgcagg tgactcag 28

<210> 51

<211> 19

<212> DNA

<213> Artificial

<220>  
<223> primer

<400> 51  
gagcatgtga ccgacattg

19

<210> 52  
<211> 30  
<212> DNA  
<213> Artificial

<220>  
<223> primer comprising BamHI site

<400> 52  
tttggatccg tcaaccagct ggtgggccag

30

<210> 53  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<223> antisense primer comprising a Sal I site

<400> 53  
aaagtcgacg tggatctcgg cctcc

25

AS/   
 <210> 54  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<223> primer

<400> 54  
tatctcgagc tgtacgtcgg tgacccc

27

<210> 55  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<223> antisense primer

<400> 55  
atatctagat cagtggatct cggcctc

27